

Application No. 09/823,649

Appendix D

(6 pages)

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entry O52225

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Entry information

Entry name DPO1_THEFI
Primary accession number O52225
Secondary accession numbers None
Integrated into Swiss-Prot on December 15, 1998
Sequence was last modified on June 1, 1998 (Sequence version 1)
Annotations were last modified on March 7, 2006 (Entry version 38)

Name and origin of the protein

Protein name DNA polymerase I, thermostable
Synonyms EC 2.7.7.7
Gene name TFI polymerase 1
Synonyms: polA
From Thermus filiformis [TaxID: 276]
Taxonomy Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae; Thermus.

References

[1] NUCLEOTIDE SEQUENCE [GENOMIC DNA].

PubMed=9509419 [NCBI, ExPASy, EBI, Israel, Japan]

Jung S.E., Choi J.J., Kim H.K., Kwon S.-T.;

"Cloning and analysis of the DNA polymerase-encoding gene from *Thermus filiformis*.";

Mol. Cells 7:769-776(1997).

Comments

- **FUNCTION:** Has 5'-to-3' exonuclease activity and no 3'-to-5' exonuclease activity.
- **CATALYTIC ACTIVITY:** Deoxynucleoside triphosphate + DNA(n) = diphosphate + DNA(n+1).
- **BIOPHYSICOCHEMICAL PROPERTIES:**
 - Temperature dependence:* Thermostable;
- **SIMILARITY:** Belongs to the DNA polymerase type-A family.
- **SIMILARITY:** Contains 1 5'-3' exonuclease domain.

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Cross-references**Sequence databases**

EMBL AF030320; AAC46079.1; -; Genomic_DNA.[EMBL / GenBank / DDBJ] [CoDingSequence]

3D structure databases

HSSP P19821; 1TAQ. [HSSP ENTRY / PDB]

ModBase Q52225.

Protein-protein interaction databases

DIP Q52225.

2D gel databases

SWISS-2DPAGE Get region on 2D PAGE.

Organism-specific gene databases

HOGENOM [Family / Alignment / Tree]

Family and domain databases

IPR002421; 5_3_exonuclease.

IPR001098; DNA_pol.

IPR002298; DNA_poll.

IPR000513; Exo_N_I.

InterPro

IPR008918; HhH2.
 IPR012337; RNaseH_fold.
 Graphical view of domain structure.
 PF01367; 5_3_exonuc; 1.
 PF02739; 5_3_exonuc_N; 1.
 PF00476; DNA_pol_A; 1.
 Pfam graphical view of domain structure.

PRINTS PR00868; DNAPOLI.

SM00475; 53EXOC; 1.

SM00279; HhH2; 1.

SM00482; POLAc; 1.

SMART graphical view of domain structure.

TIGRFAMs TIGR00593; pola; 1.

PROSITE PS00447; DNA_POLYMERASE_A; 1.

ProDom [Domain structure / List of seq. sharing at least 1 domain]

BLOCKS O52225.

Other

ProtoNet O52225.

UniRef View cluster of proteins with at least 50% / 90% / 100% identity.

Keywords

DNA damage; DNA repair; DNA replication; DNA-binding; DNA-directed DNA polymerase; Nucleotidyltransferase; Transferase.

Features



Feature table viewer



Feature aligner

Key	From	To	Length	Description	FRId
CHAIN	1	833	833	DNA polymerase I, thermostable.	PRO_0000101260
REGION	412	833	422	Polymerase (By similarity).	

Sequence information

Length: **833 AA** [This is the length of the unprocessed precursor] Molecular weight: **93891 Da** [This is the MW of the unprocessed precursor]
 CRC64: **51BF8B0417EEFC4D** [This is a checksum on the sequence]

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10	20	30	40	50	60
MTPLFDLEEP	PKRVLLVDGH	HLAYRTFYAL	SLTTSRGEFV	QMVYGFARSL	LKALKEDGQA
70	80	90	100	110	120
VVVVFDKAP	SFRHEAYEAY	KAGRAPTPE	FPRQLALVKR	LVDLLGLVRL	EAPGYEADDV
130	140	150	160	170	180
LGTLAKKAER	EGMEVRILT	DRDFFQLLSE	KVSVLLPDGT	LVTPKDVQEK	YGVPPERWVD
190	200	210	220	230	240
FRALTGDRSD	NIPGVAGIGE	KTALRLLAEW	GSVENLLKNL	DRVKPDLSRR	KIEAHLEDLH
250	260	270	280	290	300
LSLDLARIRT	DLPLEVDEKA	LRRRTPDLEG	LRAFLEELEF	GSLLEHEFGLL	GGEKPREEAP
310	320	330	340	350	360
WPPPEGAPVG	FLLSRKEPMW	AELLALAAAS	EGRVHRATSP	VEALADLKEA	RGFLAKDLAV
370	380	390	400	410	420
LALREGVALD	PTDDPLLVA	LLDPANTHPE	GVARRYGGEF	TEDAAERALL	SERLFQNLFP
430	440	450	460	470	480
RLSEKLLWLY	QEVERPLSRV	LAHMEARGVR	LDVPLLEALS	FELLEKEMERL	EGEVFRLAGH
490	500	510	520	530	540
PFNLNSRDQL	ERVLFDLGL	TPVGRTEKTG	KRSTAQGALE	ALRGAHPIVE	LILQYRELSK
550	560	570	580	590	600
LKSTYLDPLP	RLVHPRTGRL	HTRFNQTATA	TGRLSSSDPN	LQNIPTVTPPL	GQRIRKAFVA
610	620	630	640	650	660
EEGWLLLAAD	YSQIELRVLA	HLSGDENLKR	VFREGKDIHT	ETAAMMFGLD	PALVDPKMRR
670	680	690	700	710	720

```
AAKTVNFGVL YGMSAHLRSQ ELGIDYKEAE AFIERVFQSF PKVRAWIERT LEEGRTRGYV
730 740 750 760 770 780
ETLFGRRRYV PDLASRVRSV REAAERMAFN MPVQGTAAADL MKIAMVKLFP RLKPLGAHLL
790 800 810 820 830
LQVHDELVL VPEDRAEAK ALVKEVMENA YPLDVPLEVE VGVGRDNL EA KQD
```

O52225 in FASTA format

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BLAST
 BLAST submission on ExpASy/SIB
 or at NCBI (USA)



Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw,
 PeptideMass, PeptideCutter, Dotlet (Java)




ScanProsite, MotifScan



NPSA Sequence analysis tools

Submit a homology modeling request to SWISS-MODEL

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Feature aligner

Selected features of [O52225](#) (DPO1_THRF1) DNA polymerase I, thermostable (EC 2.7.7.7) (TFI polymerase 1) [Thermus filiformis].

Key Position Length Description

☐ CHAIN 1-833 833

DNA polymerase I, thermostable

MTPLFDLEEP PKRVLLVDGH HLAYRTFYAL SLTTSRGEPV QMVYGFARSL LKALKEDGQA VVVVFDKAP
SFRHEAYEAY KAGRPTPED FPRQLALVKR LVDLGLVRL EAPGYEADVV LGTLAKAER EGMVRLITG
DRDFFQLLSE RVSLLPDGT LVTPKDVQEK YGVPERWVD FRALTGDRSD NIPGVAGIGE KTAIRLLAEW
GSVENLLKNL DRVKPDSLRR KIEAHLEDLH LSLDLARIT DLPLEVDFA LRRTPDLEG LRAFLLEELEF
GSLHEFGLL GGEKPREEAP WPPPEGAFVG FLSKKEPMW AELLALAAAS EGRVHRATSP VBALADLKEA
RGFLAKDLAV LALREGVALD PTDDLLVAV LLDPANTRPE GVARRYGGEF TEDAAERALL SBRLLFQNLFP
RLSEKLLWLY QEVERPLSRV LAHNEARGVR LDVPLEALS FELKEMERL EGVFRLAGH PFNLSRDQL
ERVLFDLGL TPVGRTEKTG KRSTAQGALE ALRGHPIVE LILQVRELSK LKSTYLDPLP RLVHPRTGRL
HTRFNQTATA TGRSSSDPN LQNIPTVTPL QQRIRKAPVA EEWLALLAD YSQIELRVLA HLSGDNLKR
VFREGKDIHT ETAAMFGLD PALVDPKMR AAKTVNFGVL YGMSAHRLSQ ELGIDYKEAE AFIERVFSF
PKVRAMTERT LREGTRGYV ETLFGRRYV PDLASRVRSV REAARMFEN MPVQGTADL MKIAMVKLFP
RLKPLGAHLL LQVHDELAVLE VPEDRAEEAK ALVKEVMENA YPLDVPLEVE VGVGRDWLEA KQD

☐ REGION 412-833 422

Polymerase (By similarity)

ERLFQNLFFR LSEKLLWLYQ EVERPLSRVL AHNEARGVRL DVPLLEALSF ELEKEMERLE GEVFRLAGHP
FNLSNRDQLE RVLFDELGLT PVGRTEKTGK RSTAQGALEA LRGAHPIVE LILQVRELSK LKSTYLDPLP
LVHPRTGRLH TRFNQTATAT GRSSSDPNL QNIPTVTPLG QRIRKAPVAE EEWLALLADY SQIELRVLAH
LSGDNLKR VREGKDIHT ETAAMFGLD PALVDPKMR AAKTVNFGVL YGMSAHRLSQ ELGIDYKEAE
PIERYFSFP KVRAMTERT LREGTRGYV ETLFGRRYV PDLASRVRSV REAARMFEN MPVQGTADL MKIAMVKLFP
KIAMVKLFFR LKPLGAHLL QVHDELAVLE VPEDRAEEAK ALVKEVMENA YPLDVPLEVE VGVGRDWLEAK QD

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